



WA

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/647,140  
Source: Pu/09  
Date Processed by STIC: 6/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/647,140

DATE: 06/18/2001  
TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt  
Output Set: N:\CRF3\06182001\I647140.raw

Does Not Comply  
Corrected Diskette Needed

P.6

3 <110> APPLICANT: Fox Chase Cancer Center  
4       Kruh, Gary D.  
5       Lee, Kun  
6       Belinsky, Martin G.  
7       Bain, Lisa J.  
9 <120> TITLE OF INVENTION: MRP-Related ABC Transporter Encoding  
10      Nucleic Acids and Methods of Use Thereof  
12 <130> FILE REFERENCE: FCCC 98-02  
14 <140> CURRENT APPLICATION NUMBER: 09/647,140  
C--> 15 <141> CURRENT FILING DATE: 2001-05-21  
17 <150> PRIOR APPLICATION NUMBER: PCT/US99/06644  
18 <151> PRIOR FILING DATE: 1999-03-26  
20 <150> PRIOR APPLICATION NUMBER: 60/079,759  
21 <151> PRIOR FILING DATE: 1998-03-27  
23 <150> PRIOR APPLICATION NUMBER: 60/095,153  
24 <151> PRIOR FILING DATE: 1998-08-03  
26 <160> NUMBER OF SEQ ID NOS: 18  
28 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
31 <210> SEQ ID NO: 1  
32 <211> LENGTH: 4231  
33 <212> TYPE: DNA  
34 <213> ORGANISM: Homo sapiens  
36 <400> SEQUENCE: 1  
37 ggacaggcg ggcggccgga gccccagcat ccctgcttga ggtccaggag cggagccgc     60  
38 ggccaccgccc gcctgatcag cgcgaccgg gccccggccc gccccggccc gcaagatgct   120  
39 gcccgtgtac caggaggtga agcccaaccc gctgcaggac gcaacatct gctcacgcgt   180  
40 gttcttctgg tggctcaatc cttgtttaa aattggccat aaacggagat tagaggaaga   240  
41 tgatatgtat tcagtgcgtc cagaagaccg ctcacagcac cttggagagg agttgcaagg   300  
42 gttctggat aaagaagtta taagagctga gaatgacgca cagaagcctt ctttaacaag   360  
43 agcaatcata aagtgttact gaaaaatctta tttagttttg ggaattttta cgttaattga   420  
44 gaaaaagtgcc aaagtaatcc agcccatatt ttggggaaaa attattaatt attttggaaa   480  
45 ttatgatccc atggattctg tggctttgaa cacagcgtac gcctatgcca cggtgctgac   540  
46 ttttgcacg ctcattttgg ctatactgca tcacttatat ttttatcag ttcatgtgc   600  
47 tggatgagg ttacgatgt ccatgtgcca tatgatttat cggaggcac ttctgtcttag   660  
48 taacatggcc atggggaaa caaccacagg ccagatagtc aatctgctgt ccaatgatgt   720  
49 gaacaagttt gatcaggtga cagtgttctt acacttcctg tgggcaggac cactgcaggc   780  
50 gatcgcatgt actgcctac tctggatgga gataggaata tcgtgcctt ctggatggc   840  
51 agttctaatic attctcctgc cttgcaaaag ctgtttggg aagttgttct catcaactgag   900  
52 gagtaaaact gcaactttca cggatgcccag gatcaggacc atgaatgaag ttataactgg   960  
53 tataaggata ataaaaatgt acgcctggaa aaagtcattt tcaaatttta ttaccaattt   1020  
54 gagaaaagaag gagatttcca agattctgag aagtccctgc ctcaggggga tgaatttggc   1080  
55 ttctgttttc agtgcagca aatcatctgt gtttgtgacc ttccaccacct acgtgctcct   1140  
56 cggcagtgtg atcacagcca gcccgtgtt cgtgcagtg acgctgtatg gggctgtgcg   1200  
57 gctgacgggtt accctcttct tcccctcagc cattgagagg gtgtcagagg caatcgtcag   1260  
58 catccgaaga atccagacct ttttgcatact tgatgagata tcacagcgc accgtcagct   1320  
59 gccgtcagat ggtaaaaaga tggtgcatgt gcaggatttt actgctttt gggataaggc   1380  
60 atcagagacc ccaactctac aaggccttc cttaactgtc agacctggcg aattgttagc   1440

## **RAW SEQUENCE LISTING**

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Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

RAW SEQUENCE LISTING  
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Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt  
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112 <212> TYPE: PRT  
 113 <213> ORGANISM: Homo sapiens  
 115 <400> SEQUENCE: 2  
 116 Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala  
 117 1 5 10 15  
 118 Asn Ile Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys  
 119 20 25 30  
 120 Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu  
 121 35 40 45  
 122 Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp  
 123 50 55 60  
 124 Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu  
 125 65 70 75 80  
 127 Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly  
 128 85 90 95  
 129 Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe  
 130 100 105 110  
 131 Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser  
 132 115 120 125  
 133 Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys  
 134 130 135 140  
 135 Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln  
 136 145 150 155 160  
 137 Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg  
 138 165 170 175  
 139 Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Gly  
 140 180 185 190  
 141 Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val  
 142 195 200 205  
 143 Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala  
 144 210 215 220  
 145 Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly  
 146 225 230 235 240  
 147 Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys  
 148 245 250 255  
 149 Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg  
 150 260 265 270  
 151 Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met  
 152 275 280 285  
 153 Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys  
 154 290 295 300  
 155 Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn  
 156 305 310 315 320  
 157 Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe  
 158 325 330 335  
 159 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe  
 160 340 345 350  
 161 Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe  
 162 355 360 365

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```

 163 Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
 164      370          375          380
 165 Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
 166      385          390          395          400
 167 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
 168      405          410          415
 169 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
 170      420          425          430
 171 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
 172      435          440          445
 173 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
 174      450          455          460
 175 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
 176      465          470          475          480
 177 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
 178      485          490          495
 179 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
 180      500          505          510
 181 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
 182      515          520          525
 183 Gly Asp Arg Gly Thr Pro Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
 184      530          535          540
 185 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
 186      545          550          555          560
 187 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
 188      565          570          575
 190 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
 191      580          585          590
 192 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
 193      595          600          605
 194 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
 195      610          615          620
 196 Ile Asp Phe Gly Ser Leu Leu Lys Asp Asn Glu Glu Ser Glu Gln
 197      625          630          635          640
 198 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
 199      645          650          655
 200 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
 201      660          665          670
 202 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
 203      675          680          685
 204 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
 205      690          695          700
 206 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
 207      705          710          715          720
 208 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
 209      725          730          735
 210 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
 211      740          745          750
 212 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr

```

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**DATE: 06/18/2001**  
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213	755	760	765
214	Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu		
215	770	775	780
216	Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys		
217	785	790	795
218	Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn		800
219	805	810	815
220	Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu		
221	820	825	830
222	Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu		
223	835	840	845
224	Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile		
225	850	855	860
226	Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg		
227	865	870	875
228	Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr		
229	885	890	895
230	Arg Ser Pro Val Phe Ser His Leu Ser Ser Leu Gln Gly Leu Trp		
231	900	905	910
232	Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp		
233	915	920	925
234	Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr		
235	930	935	940
236	Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val		
237	945	950	955
238	Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala		
239	965	970	975
240	Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met		
241	980	985	990
242	Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile		
243	995	1000	1005
244	Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro		
245	1010	1015	1020
246	Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val		
247	1025	1030	1035
248	Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu		
249	1045	1050	1055
250	Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly		
251	1060	1065	1070
253	Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu		
254	1075	1080	1085
255	Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu		
256	1090	1095	1100
257	Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile		
258	1105	1110	1115
259	Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp		
260	1125	1130	1135
261	Pro Phe Lys Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Arg Glu		
262	1140	1145	1150

09/647,140

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<210> 9  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Sequence source:/note="synthetic construct"

<400> 9

ctdgtdgcdg tdgtdgg

*see item 9 on Seq Summary sheet*

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 06/18/2001  
PATENT APPLICATION: US/09/647,140 TIME: 16:26:36

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt  
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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1174 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9  
L:1174 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9  
L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:1259 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16  
L:1259 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16  
L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:1270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17  
L:1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17  
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18  
L:1282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18  
L:1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18